

FIG.1

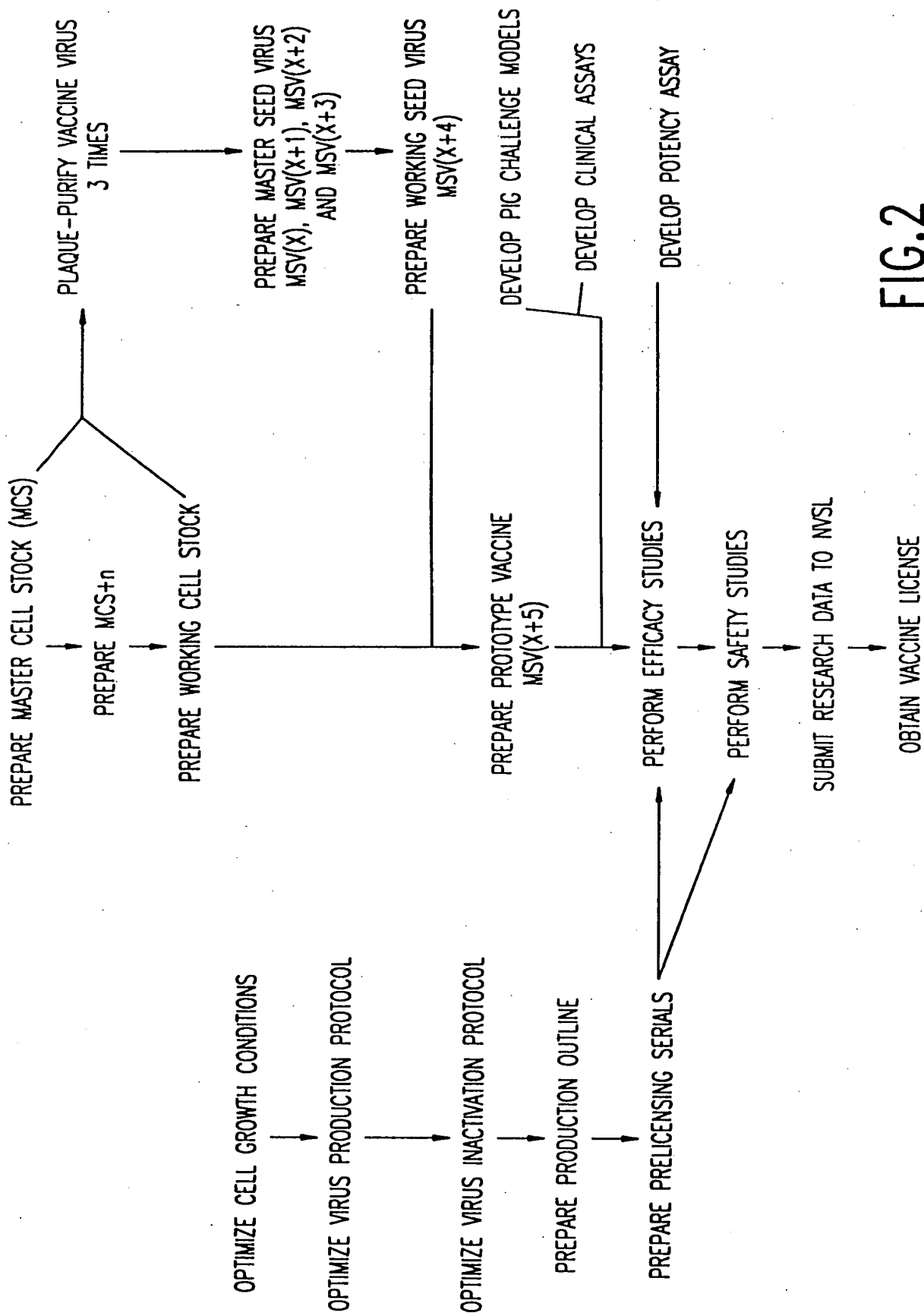
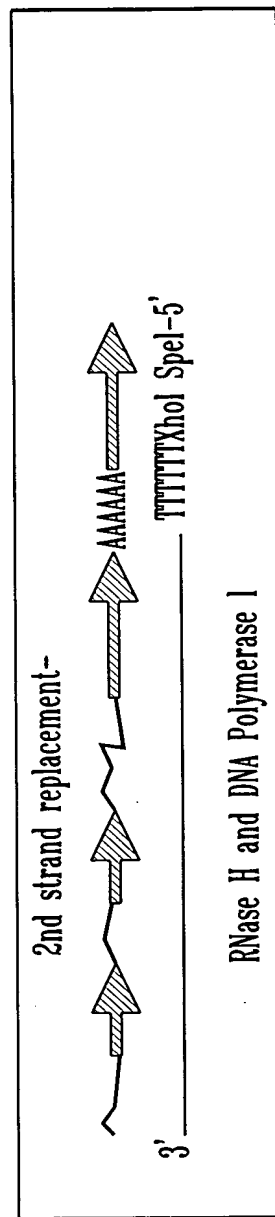
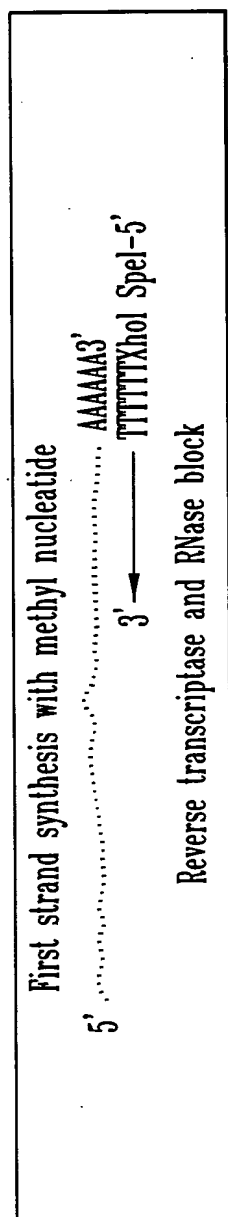


FIG. 2



↓
To Fig.3b

FIG. 3A

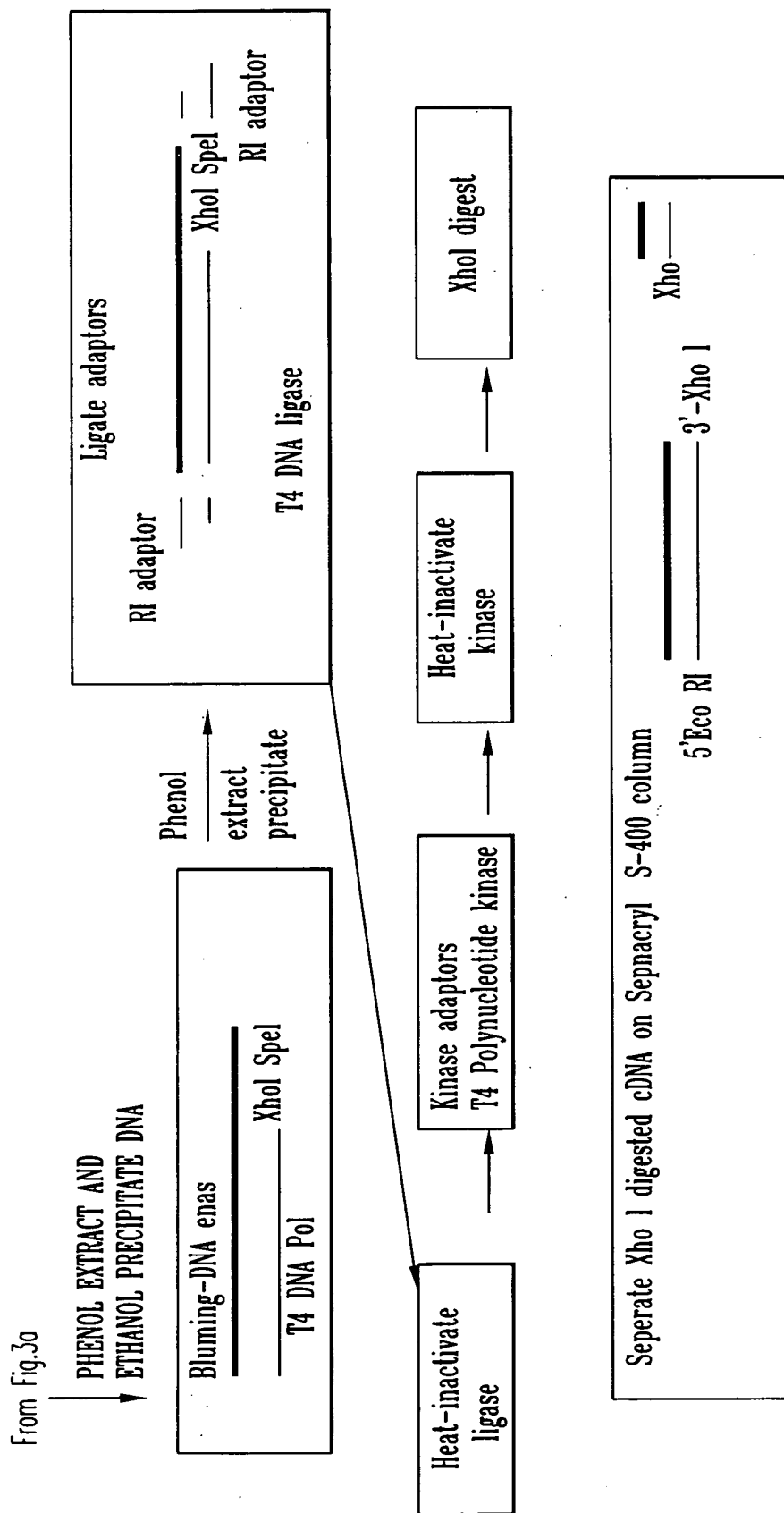


FIG. 3B

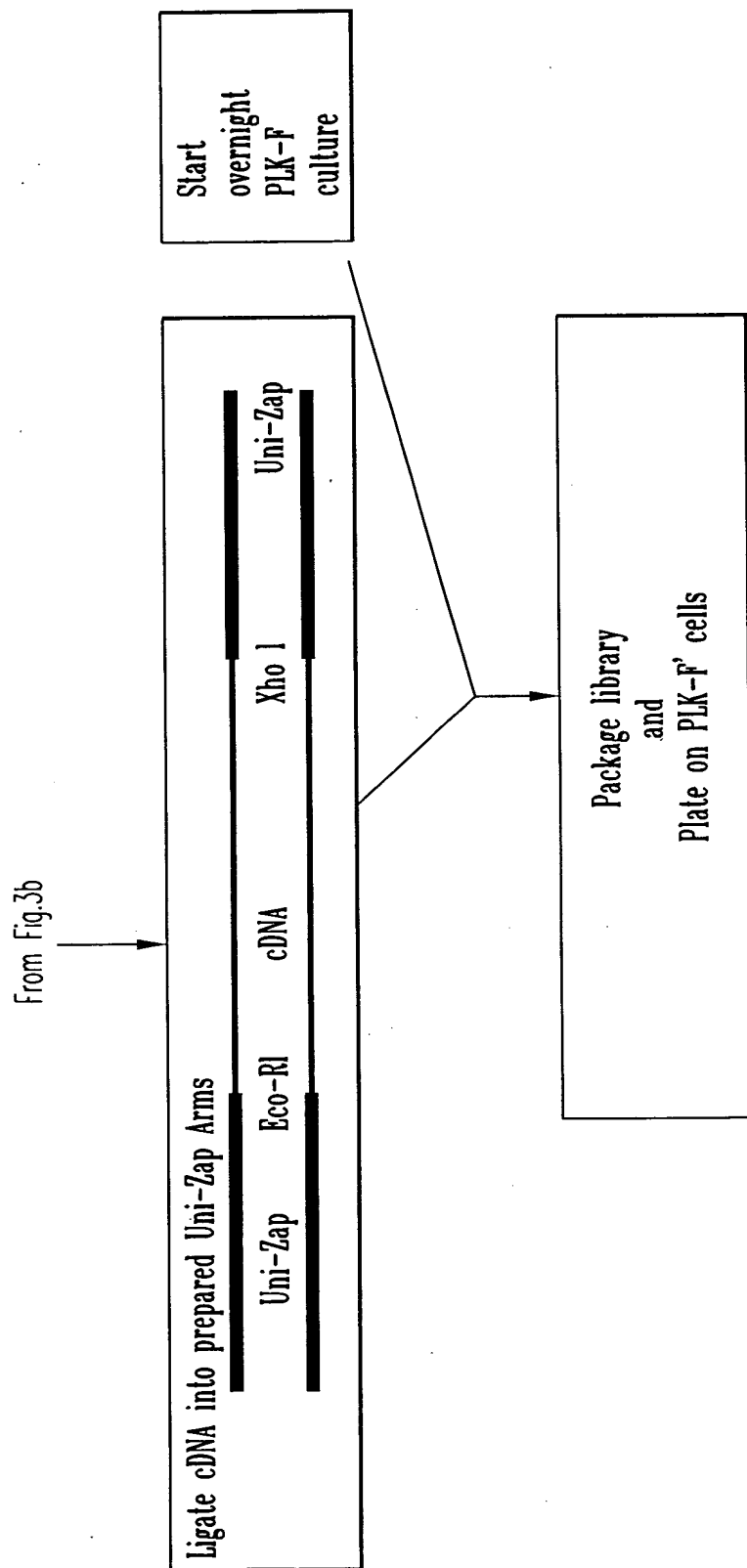


FIG. 3c

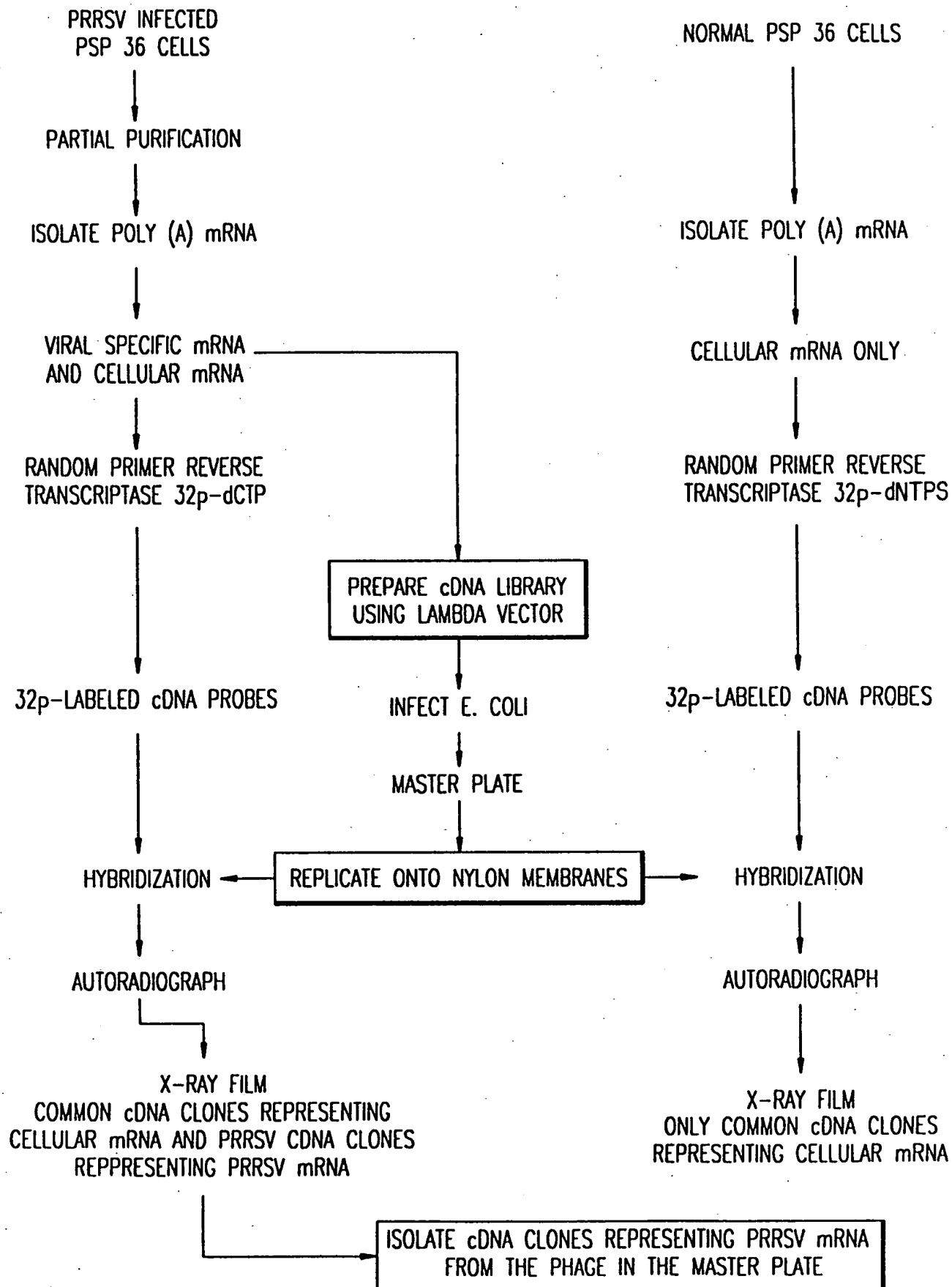


FIG.4

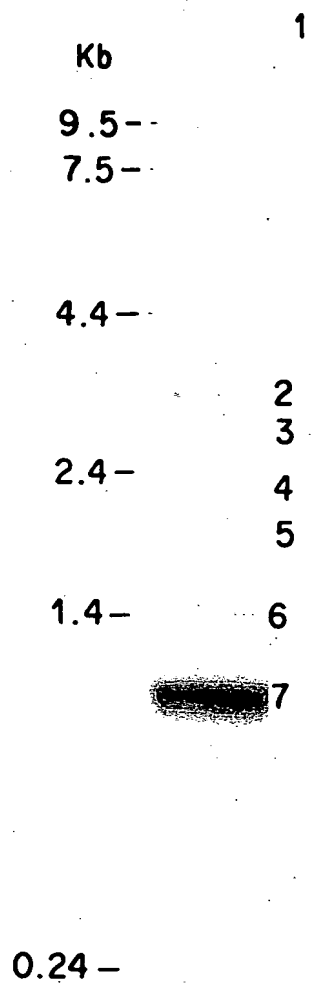


FIG.5

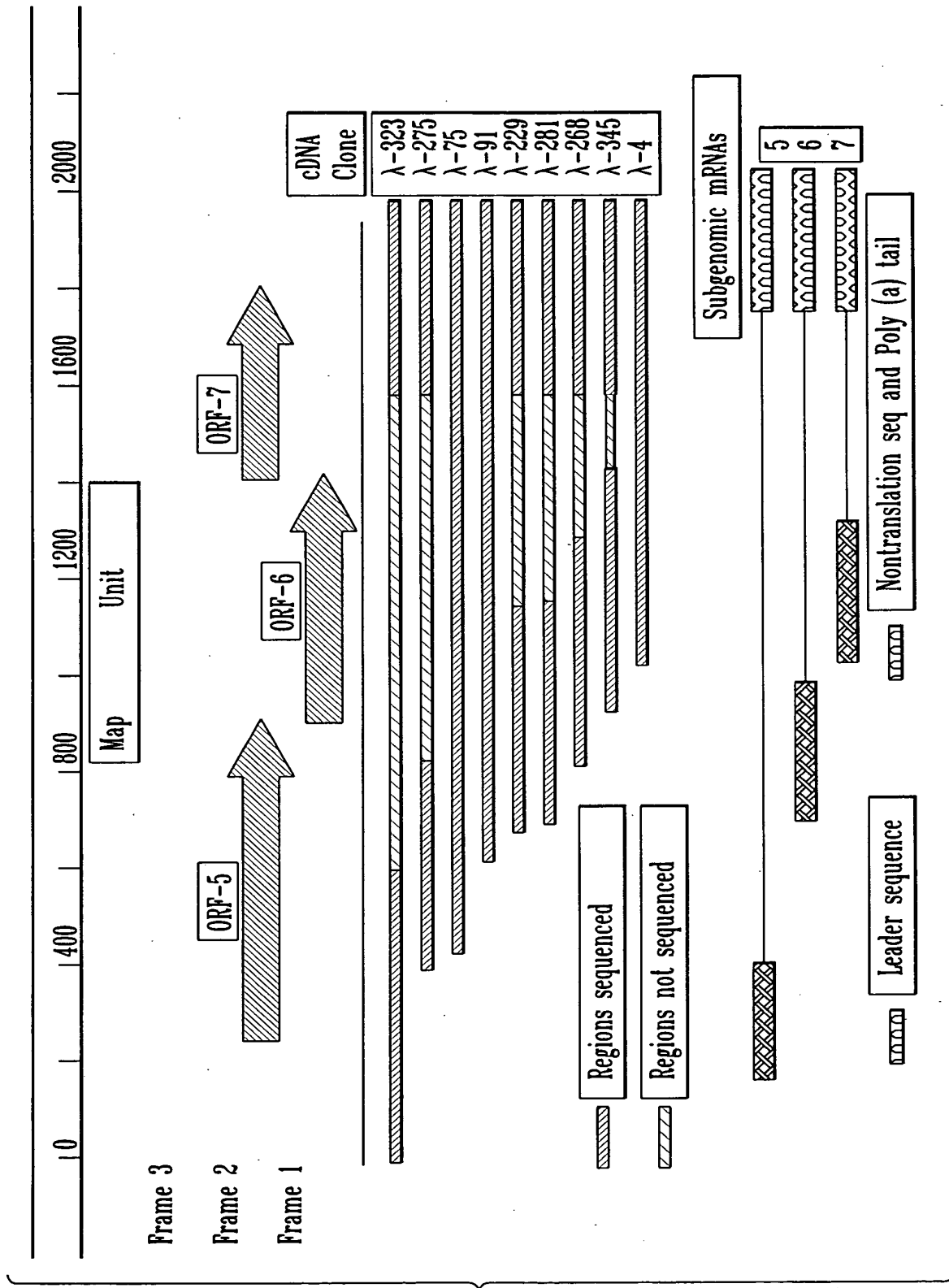


FIG. 6


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GGCAGGCTTTGCTGCTCCTCCAAAGACATCAGTTGCCTTAGGCATCGCAACTGGCCCTCTAGGGCGATTCCGAAAGTCCCTCAGTGCCGCACGGCGATAGGG 100
ACACCCGTGTATACACTGTCACAGCCCAATGTTACCGATGAGAAATTATTGCATTCCCTCIGATCTTCTCATGCTTTCTTCTTGCCTTTCTATGCTTCTG 200
AGATGAGTGAAAAGGGATTAAAGGTGGTATTTGGCAA TGTCAGGGATCGTGGCAGTGTCGCTCAACTTCACCAGTTACGTCCAACATGTC AAGGAATT 300
TACCAACGTTCCTTGGTAGTTGACCATGTGCGGCTGCTCCATTTTCATGACGCCCGAGACCATGAGGTGGGCAACTGTTTTAGCCTGTC TTTTTTGGCATT 400
DRF4 stop
*** +1>DRF5 start
CTGTTGGCAATTGAATGTTAAGTATGTTGGGAAATGCTTGACCGCGGGCTGTTGCTCGCAATTGCTTTTTTGGTGATCGTGCCGCTTGTTTT 500
GTTGCGCTCGTCAGCGCCAACGGGAACAGCGGCTCAAAATTACAGCTGATTTACAAC TTGACGCTA GTGAGCTGAATGGCACAGATTGGCTAGCTAATA 600
AATTGACTGGGCAGTGGAGTGTTTGTGCATTTTTCCTGTTGACTCAGATTGTCCTTATGGTGCCCTCAGTACTAGCCATTTCCTTGACACAGTCGG 700
TCTGGTCACTGTGCTACCGCTGGGTTGTTACGGGGGGTATGTTCTAGTAGCATGTACGGGCTCTGTCCTGGCTGGCTGGATTGCTTCGTCATT 800
AGGCTTGCGAAGAA TTGCA TGTCCTGGCGCTACTCATGTACCAGATATACCAACTTCTTCTGGACACTAAGGGCAGACTCTATCGTTGGCGGTGCGCTG 900
TCATCATAGAGAAAGGGGCAAGTTGAGGTGGAAGGTCACCTGATCGACCTCAAAAGAGTTGTGCTTGATGGTTCGCGGGCTACCCCTGTACCAGAGT 1000
DRF6 start
+1> ***DRF5 stop
TTCACGGGAACAAATGGAGTCGTCCTTAGATGACTTCTGTCATGATAGCAGGCTCCACAAAGGTGCCTTGCGGTTTTCTATTACCTACACGCCAGTGA 1100

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FIG. 7A

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TGATATATGCCCTAAAGGTGAGTCGCGCGGCGACTGCTAGGGCTTCGACACCTTTGGCTCTCCTGAAATTGTGCTTTCACCTTCGGGTACATGACATTCGT 1200

GCAC TTCAGAGTACAAATAAGGTCGCGCTCACTATGGGAGCAGTAGTTGCAC TCCTTTGGGGGGGTGTA CTAGCCATAGAAACCTGGAAATTCATCACC 1300

TCCAGATGCCGCTTTGTGCTTGCTAGCGCGCAAGTACATTCTGGCCCTGCCACCACGTTGAAAGTGCCGAGGCTTTCATCCGATTGGCGCAATGATA 1400

ACCACGCATTTGTCGTCGGGCTCCCGGCTCCACTACGGTCAACGGCACATTGGTGCCCGGGTTAAAAAGCCTCGTGTGGGTGGCAGAAAAGCTGTTAA 1500
      DRF7 start
      +1> ***DRF6 stop
ACAGGGAGTGGTAAACCTTGTTAATAATGCCAAATAACACCGGCAAGCAGCAGAGAGAGAAAGAGGGGGATGGCCAGCCAGTCAATCAGCTGTGCCAGAT 1600

GCTGGGTAAAGTATCGCTCACCAAAACCAGTCCAGAGGGCAAGGACCGGGAAAGAAAAATAAGAGAAAAAACCCGGAGAGCCCCATTTCCTCTAGCG 1700

ACTGAAGATGATGTCAGACATCATTACCCCTAGTGAGGCTCAATTGTGCTGTCATCCAGACCGCCTTAAATCAAGGGCTGGGACTTGCACCC 1800
      ***DRF7 stop
TGTGAGATTCAGGGAGGATAAGTTACACTGTGGAGTTTAGTTTGCTACGCATCATACTGTGGCCTGATCCGGGTACAGCATCACCCCTCAGCATGATG 1900

GGCTGGCATTCTTGAGGCATCCAGTGTGTGAATTGGAAGATGGGTGGTGAATGGCACGTGATTGACATTGTGCCTCTAAGTCACCTATTCAATTAGGGC 2000

GACCGTGTGGGGGTAAGATTTAATTGGCGAGAACCCACACGCGCGAAATTAATAAAAAAAAAA 2062

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FIG. 7B

LELYSTAD SEQ (13484-14089)	ATGAGATGTTCTCACAAATGGGGCGTTTCTTGACTCCGCACCTCTTGGCTTCTGGTGGCTTTTTTTCGCTGIGTA--	13556
ISU-12-3' TERMINAL (426-1028)	-----ATGTGGGGAATTCCTTGACCCGGCTCTTGGCTCGCAATTTGCTTTTTTGTGGGTATC	485
LELYSTAD SEQ (13484-14089)	---CCGCTTGTCCTGGT-CCTTTGGGATGGCAACGGCCACAGCTCGACATACCATAA-C-ATAATATAACTTG	13624
ISU-12-3' TERMINAL (426-1028)	GTCCCTCTTGTTTCTGGCTCTGAGCCCAACGGGAACAGGGCTCAAAATTACAGCTGATTTACAACTTG	560
LELYSTAD SEQ (13484-14089)	ACGATATGGAGCTGAATGGACCGACTGGTTGTCCAGCCATTTTGGTTGGGCAGTGGAGACCTTTGTGCTTTAC	13699
ISU-12-3' TERMINAL (426-1028)	ACGCTATGTGAGCTGAATGGACAGATTGGCTAGCTAATAAATTTGACTGGGCAGTGGAGTGTTTTGTCATTTTT	635
LELYSTAD SEQ (13484-14089)	CCGGTTGCCACTCATAATCCCTCTCACTGGGTTTCTCACAAAGGCCATTTTGTGACGGCTCGGCTCTGGGCTCT	13774
ISU-12-3' TERMINAL (426-1028)	CCGTGTTGACTCACAATGTCCTCTTATGGTGGCTCACCTACTAGCCATTTCCTTGACACAGTCCGCTCTGGTCACT	710
LELYSTAD SEQ (13484-14089)	GTAATCCACTGCAAGATTGTTGTTGGGGGCGGTAGGTACTCTGCAGCTCTACGGCTTTGTGGCTTTGCGAGCGGTTC	13849
ISU-12-3' TERMINAL (426-1028)	GTGCTACCGCTGGTTTGTTCACGGGCGGTATGTTCTGAGTAGCAATGACCGCTGTGGCCCTGGCTGGCTTG	785
LELYSTAD SEQ (13484-14089)	GTATGTTTGTTCATCCGTGCTGCTGAATAATTGCAATGGCTCCGGCTATGCCGTACCGGTTTACCAACTTCATT	13924
ISU-12-3' TERMINAL (426-1028)	AATTTGCTTGGTCAATAGGCTTGGCAAGCAATTGCAATGCTCCGCGCTACTGATGACCAAGATATACCAACTTTCTT	860
LELYSTAD SEQ (13484-14089)	GTGGACGACCGGGGAGAGTTTCATCGATTGGAAGTCTCCAAATAGTGGTAGAATAATTTGGGCAAGCCGAAAGTGGAT	13999
ISU-12-3' TERMINAL (426-1028)	CTGGACACTAAGGGCAGACTCTATCGTTGGCGGTCCGCTGTCATCATTAGCAAAAGGGGCAAAAGTTGAGGTCCGAA	935
LELYSTAD SEQ (13484-14089)	GGCAACCTCGTCAACCAATCAAAACATGTGCTCTCGAAGGGGTTAAAGCTCAACCCCTTTGACGAGGACTTCGGGTGA	14073
ISU-12-3' TERMINAL (426-1028)	GGTCACCTGATCGACCTCAAAAGAGTTGTGCTTGATGTTCCGGCGCT-ACCCCTGTAAACCACAGTTTCAGGGGA	1009
LELYSTAD SEQ (13484-14089)	GCAATGGGAGCCCTAG-----	14089
ISU-12-3' TERMINAL (426-1028)	ACAAATGGAGTCTCCCTTAG	1028

FIG. 8

ISU 12/7a/3' terminal (888 – 1413)	AATGGAGTGG TCGTTAGATG ACTTGTGTCA TGATAGCAGG GGTCCACAAA AGGTGCTCTT	947
LeIystad seq (14077 – 14598)	-ATGG-GACG --CGTACAGG ATTITTTGCAA CGATCCTATC GCGGCACAAA AGCTCGTGGT	14132
ISU 12/7a/3' terminal (888 – 1413)	GGCGTTTCT ATTAACCTACA GCGCAGTAT GATATATGCC CTAAAGGTGA GTCCCGGCGG	1007
LeIystad seq (14077 – 14598)	AGCGTTTACG ATACACATACA CACGTATTAAT GATATAAGCC CTAAAGGTGT CACCGGCGCGG	14192
ISU 12/7a/3' terminal (888 – 1413)	ACTGCTAGGG CTTCGTGACC TTTTGGTCTT CTGAATTTGT GCTTTCACT TCGGATACAT	1067
LeIystad seq (14077 – 14598)	ACTGCTAGGG CTTCGTGACA TCGTAATTAAT TCTGAACITGT TCGTTTACAT TCGGATACAT	14252
ISU 12/7a/3' terminal (888 – 1413)	GACATTCGTG CACTTTCAGA GTACAATAA GTTCGGGCTC ACTATGGGAG CAGTAGTTGC	1127
LeIystad seq (14077 – 14598)	GACATATGTG CATTTTCAAT CCACCAACCG TGTCCGACIT ACCGTGGCGG GTGTTGCTGG-	14311
ISU 12/7a/3' terminal (888 – 1413)	ACTCCTTTGG GGGGTGTAAT CAGG-CATA GAAACCTGGA AATTCAATCAC CTCCAGATGC	1185
LeIystad seq (14077 – 14598)	-CCCTTTCTGT GGGGTGTTTA CAGCTTCACA GAGTCAATGGA AGTTTATCAC TTCCAGATGC	14370
ISU 12/7a/3' terminal (888 – 1413)	CGTTTGTGCT TGTAGGCGG CAAGTACATT CTGGCCCCCTG CCCACACAGT TGAAGTGGC	1245
LeIystad seq (14077 – 14598)	AGATTGTGTT GCCTTGGCGG GCGATACATT CTGGCCCCCTG CCCATCACGT AGAAGTGGT	14430
ISU 12/7a/3' terminal (888 – 1413)	GCAGGCTTTC ATCCGATTC GCGAAATGAT AACCAAGCAT TTGTGCTCGG GCGTCCCGGC	1305
LeIystad seq (14077 – 14598)	GCAGGTCTCC ATTCAATCTC AGGTGTGTT AACCGAGCAT ACGCTGTGAG AAAGCCCGGA	14490
ISU 12/7a/3' terminal (888 – 1413)	TCCACTACCG TCAACGGCAC ATTGCTCCC GGGTTAAATA GCCTCGTGT TGGTGGCAGA	1365
LeIystad seq (14077 – 14598)	CTAACAATAG TGAACGGCAC TGTAGTACCA GGAATTCGGA GCCTCGTGT GGGCGGCANA	14550
ISU 12/7a/3' terminal (888 – 1413)	AAGCTGTTA AACAGGAGT GGTAAACCTT GTTAATATATG CCAATATA	1413
LeIystad seq (14077 – 14598)	CGAGCTGTTA AACAGGAGT GGTAAACCTC GTTAATATATG GCGGTATA	14598

FIG. 9

Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	ATGGCCGGTA AAACCAAGAT- -----AT GCCAAGAGAA GCCAATATAC ACCGCAAGC AGCAGAAGAG	14632 14634
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TCCGATGGGG AATGGCCAGC CAGTCAATCA AAACAAGGGG GATGGCCAGC CAGTCAATCA	14681 1483
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	CAATGATAAA GTCCACGGC CACCAACCTA -AA-CATCAT CCGTCACGAA AACAGTCCA GAGGCAAGG ACCGG--GA	14728 1528
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	AAGAAAAA-- AAGAAAAATA AGAAGAAAAA CCCGGAGAAG CCGCATTTCC CTCTAGCGAG	14766 1578
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TGAAGATGAC ATCCGGCACC AACTACCCA TGAAGATGAT GTCAACATTC ACTTTACCCC TAGTGACCGT CAATTGTGTC	14816 1628
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TGCAATCGAT CCAGACGGGT TGTCGTGAT CCAGACCGCC TTTAAATCAAG GCGCTGGCAG	14865 1677
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TTTCATCCAGC GGGAGGTCA GTTTTCAGGT GTCAGATTCA GGGAGGATAA GTTACACTGT GGAGTTTATG GTCCGGTTG TTCCGTACGC	14915 1727
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	CTCATACAGT GCGCTGATTT ATCATACTGT GCGCTGATC CGCGTACAG CATACCC-T CAG-CATGA-	14965 1774
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	GCAAGTTAA	14974 1774

FIG.10

ISU 12/7a/3' terminal (1775 – 1938)	1814
Lelystad seq (14975 – 15101)	14976
	TGGCTGGCA TTCTTGGGC ATCCAGTGT TTGAATGGCA -----TT
ISU 12/7a/3' terminal (1775 – 1938)	1854
Lelystad seq (14975 – 15101)	15016
	AGAATGGTGTGTGTGAATGGCA CTGATTGACA TTGTGCCTCT TGACAGTCAG GTGAATGGCC GCGATTGGCG TTGTGCCTCT
ISU 12/7a/3' terminal (1775 – 1938)	1800
Lelystad seq (14975 – 15101)	15056
	AGTCACCTA TTCAATTAGG GCGACCGTGT GGGGGTACGA GAGTCACCTA TTCAATTAGG GCGATCACAT GGGGGTCAATA
ISU 12/7a/3' terminal (1775 – 1938)	1933
Lelystad seq (14975 – 15101)	15096
	TTTAATTGG CGACAACCAC ACAGCCGAAA TTAAAAAAA GTTAATCAGG CAGCAACCAT GTACCCGAAA TTAAAAAAA
ISU 12/7a/3' terminal (1775 – 1938)	1938
Lelystad seq (14975 – 15101)	15101
	AAAAA AAAAA

FIG. 11

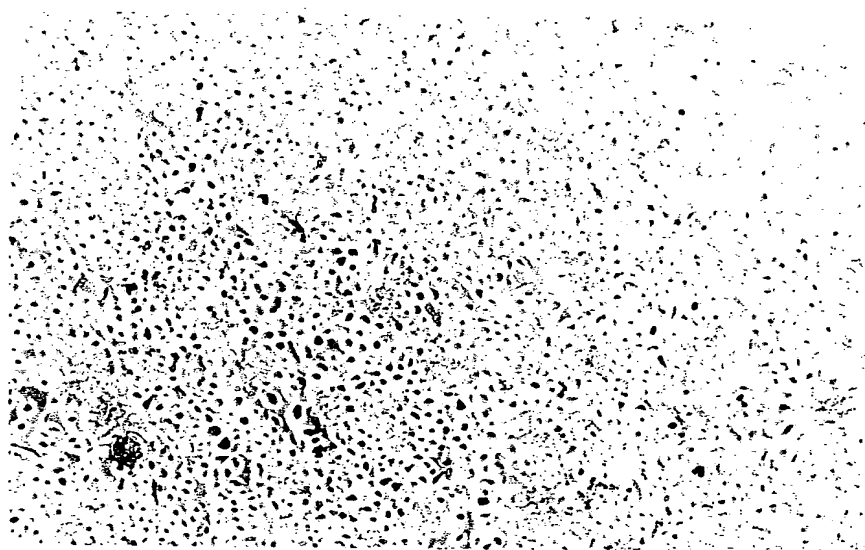


FIG.12

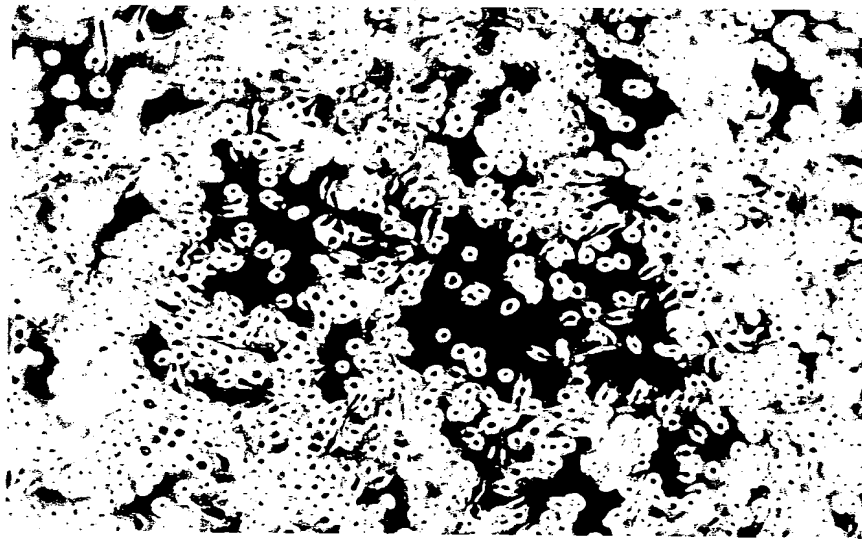


FIG.13

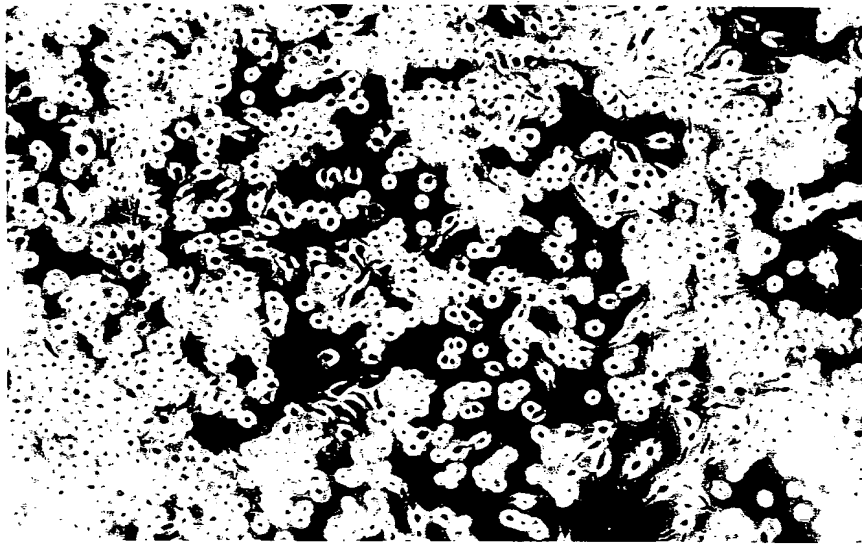


FIG.14

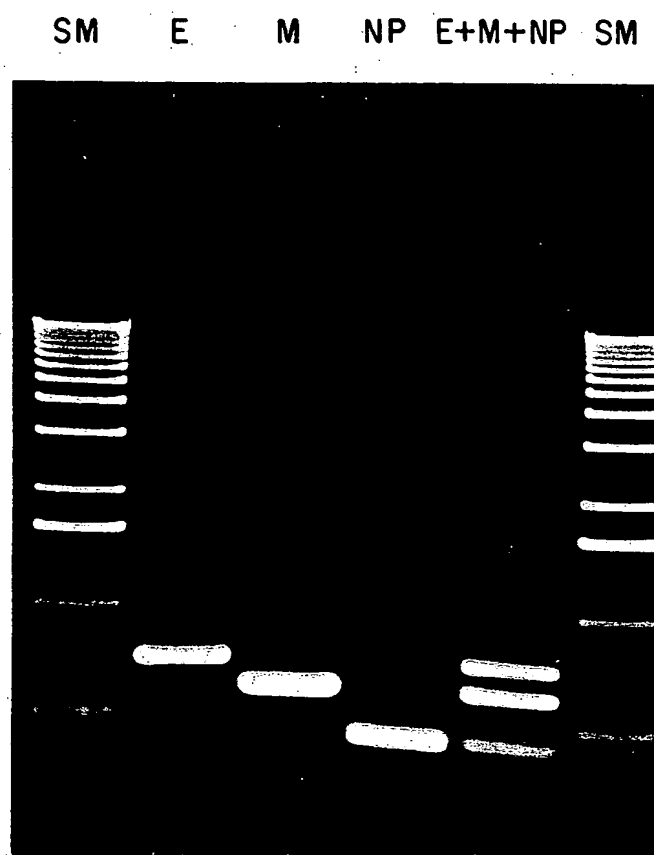


FIG.15

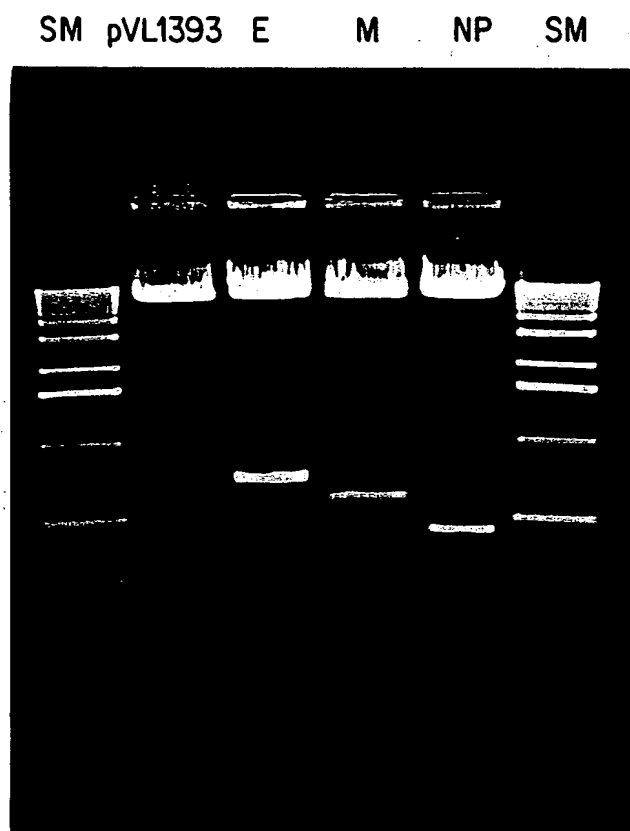


FIG.16

DRF 6 start
+ 1>

VR 2385	AI	G	G	A	G	T	C	G	T	C	T	T	A	G	A	T	G	A	T	G	A	T	G	A	T	G	C	C	100
ISU-1894	100
ISU-22	100
ISU-79	100
ISU-55	100
ISU-3927	100
LV	97

VR 2385	T	A	A	G	G	T	A	G	T	C	G	G	C	G	A	C	T	T	T	G	G	T	C	T	T	C	C	T	T	200
ISU-1894	200
ISU-22	200
ISU-79	200
ISU-55	200
ISU-3927	200
LV	197

VR 2385	T	A	C	A	A	T	A	G	G	T	C	G	G	C	T	C	A	T	A	G	A	G	C	A	T	G	A	T	G	298
ISU-1894	298
ISU-22	298
ISU-79	298
ISU-55	298
ISU-3927	298
LV	295

FIG. 17A

VR 2385	CCAGATGCTGGGT--AA-GATCATCGCTACCAAAACCAAGTCCAGAGGCAAGGACCGGGAAAGAAAAATAAGAGAAAAACCCGGAGAGCCCCATTTC	679
ISU-1894--,. .G.....C.....T	679
ISU-22C--,. .G....T.....	679
ISU-79--,. .C.G.....T.....	679
ISU-55--,. .G.....C.....	679
ISU-3927	...A.....--,. .C.G.....T.....	679
LVGC..T...A.AGT..C..G.---G....-,. .-,. .CCT..G....C...---GCC..A.....G..T.....A.....T	679

VR 2385	CCTCTAGCGACTGAAGATGATGTCAGACATCACTTACCCCTAGTAGGCGTCAATTGTGTCTGTCTCAATCCAGACCGCCTTTAATCAAGGCGCTGGGA	779
ISU-1894C.....C.....G.....	779
ISU-22G.....G.....	779
ISU-79G.....G.....A..T.....	779
ISU-55C..T..G.....G.....A.....A.....	779
ISU-3927C.....C.....C.....G.....T.....G.....	779
LV	..C..G..TG.....CA..C.G..C...C.C...AG.C...A..CTCCC.C..CT..CAA..G.....G..T..C.....A..A.....	779

FIG. 17C

VR 2385	CTTGACC-CTGTCAGATT	CAGGAGGATAAGTTACACTGTGGAGTTAGTTGGCTACGCATCATACTGTGGCCTGATCCGGTCACAGCATCACCC-	877
ISU-1894A.....T.....	877
ISU-22	877
ISU-79T.....	877
ISU-55T.....G.....G.....	877
ISU-3927C..T.T..A.....G.....T.....G..C.....	877
LVGT.G..T...TCCAGC...TGC...GGTTGC.....A.....G..TT.TA..T..G	878

VR 23 85	TCAG-CA-----TGA	886
ISU-1894	886
ISU-22	886
ISU-79	886
ISU-55	886
ISU-3927	886
LV	C...T..GGGTGCAAGT.A. ^^^^^^^^^^	898

FIG. 17D

VR 2385 DRF6	MESSLDDFCHDSTAPQKVLLAFSITTPVMIYALKVSRGRLLGLLHLLVFLNCAFTFGYMTFVHFQSTNKVALTMGAVVALLWGVYSAIETWKFITSRCR	100
ISU-1894 DRF6	.G.....I.....	100
ISU-22 DRF6	.G.....I.....	100
SIU-55 DRF6	.G.....I.....	100
ISU-79 DRF6	.G.....Y.....M.....	100
ISU-3927 DRF6	.G.....N.....I.....E..R.....	100
LV DRF6	.G-G.....N.PI.A..LV.....I.....S.....Y.....R....L.....FT.S.....	99
PRRSV-10 DRF6	.G-G.....N.PI.A..LV.....I.....S.....Y.....R....L.....FT.S.....	99
LDV-C DRF2	.G-G.-E..DQTSWY.-IFI..L....IA..S...F..T.A.IVNIFI..I..CVS.V.LMYH.-SV..TI..SL...I..V..I.TLVKIVDVLVI...	96
LDV-P DRF2	.G-G.-E..DQTSWY.-I..I...L....IA..S...F..T.A.IVNIFI..I..CVS.V.LMYH.-SV..T...SL...I..V..I.TLVKIVNMVVL...	96

VR 2385 DRF6	LCLLGRKYILAPAHHVESAAAGFHPAANDNH-----AFVVRPRPGSTTVNGTLVPGLKSLVLGGRKAVKQGVVNLVKY-AK	183
ISU-1894 DRF6-----.....	174
ISU-22 DRF6-----.....	174
SIU-55 DRF6-----.....	174
ISU-79 DRF6-----.....	174
ISU-3927 DRF6-----R.....K.....	174
LV DRF6	.C...R.....L.S.S.SG.R-----YA.K..L.S.....R.....KR..R.....-GR	173
PRRSV-10 DRF6	.C...R.....L.S.S.SG.R-----YA.K..L.S.....R.....KR..R.....-GR	173
LDV-C DRF2	.F...S....PS.,D-----TSDGRQSLTTSITT.....K...L...Q...DFQR.....K...SK.A...L...VS,	171
LDV-P DRF2	.F...S....PS.,D-----TSDGRQSLTTSITT.....K...L...Q...DFQR.....K...SK.A...L...VS,	171

FIG. 18A

VR 2385 DRF7	MPNNTGKQQRKK-----GDGQPVNQLCQMLGKIIAHQNSRGKGPCKKNKKKNPEKPHFPLATEDDDVRHHFTPSERQLCLSSIQTAFNQAGTCTLS	100
ISU-1894 DRF7N.....Q.....	93
ISU-22 DRF7N.....Q.....	93
ISU-79 DRF7N.....Q.....	93
ISU-3927 DRF7N.....K.....Q.....I..	93
ISU-55 DRF7N.....K.....Q.....SG.....	93
VR2332 DRF7N...TEE.....Q.....	93
LV DRF7-A..N.SQ.,KKSTAPM,N.....L..AM.KS.R.---QPR.GQA...K.....A...I...L.QT...S...Q.....AS..	94
PRRSV-10 DRF7-A..N.SQ.,KKSTAPM,N.....L..AM.KS.R.---QPR.GQA...K.....A...I...L.QT...S...Q.....PS..	94
LDV-C DRF1	..SQ.KK.GGQN-----AN,---,N.LISALLRNAG,--N..K.Q.K.-Q.-L...M.GPS,L.,VM..N.V.M.R.,LV,L.,...G.Q.,,V	85
LDV-P DRF1	..SQ.KK.SGQN-----AN,---,N.LINALLRNAG,--N..K.Q.K.-Q.-L...M.GPS,L.,VM..N.V.M.R.,LV,L.,...G.Q.,,V	85
EAV DRF7	..ASRRSRP,AASF-----RN,R--RRQPTSYNLLRMFG,-----MRVR.PPAQPTQATI,EPG,L.,DLNQQ.,ATLS.NV.RF.MI.H.SL.-A	83

^^^^^^

VR 2385 DRF7	DSGRISYTFEFSLPTHHTVRLIRVTASP-----SA	134
ISU-1894 DRF7	123
ISU-22 DRF7	123
ISU-79 DRF7	123
ISU-3927 DRF7P,-----	123
ISU-55 DRF7	123
VR2332 DRF7	123
LV DRF7	S.,KV.FQ...M.,VA.....STSASQGAS	128
PRRSV-10 DRF7	S.,KV.FQ...M.,VA.....STSASQGAS	128
LDV-C DRF1	...G.NF..S.M.,A.....NAS,NS-----	115
LDV-P DRF1	...G.NF..S.M.,A.....NAS,NS-----	115
EAV DRF7	A.GLT,...SW-V.,KQIQ.KVAPP,G,-----	110

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FIG. 18B

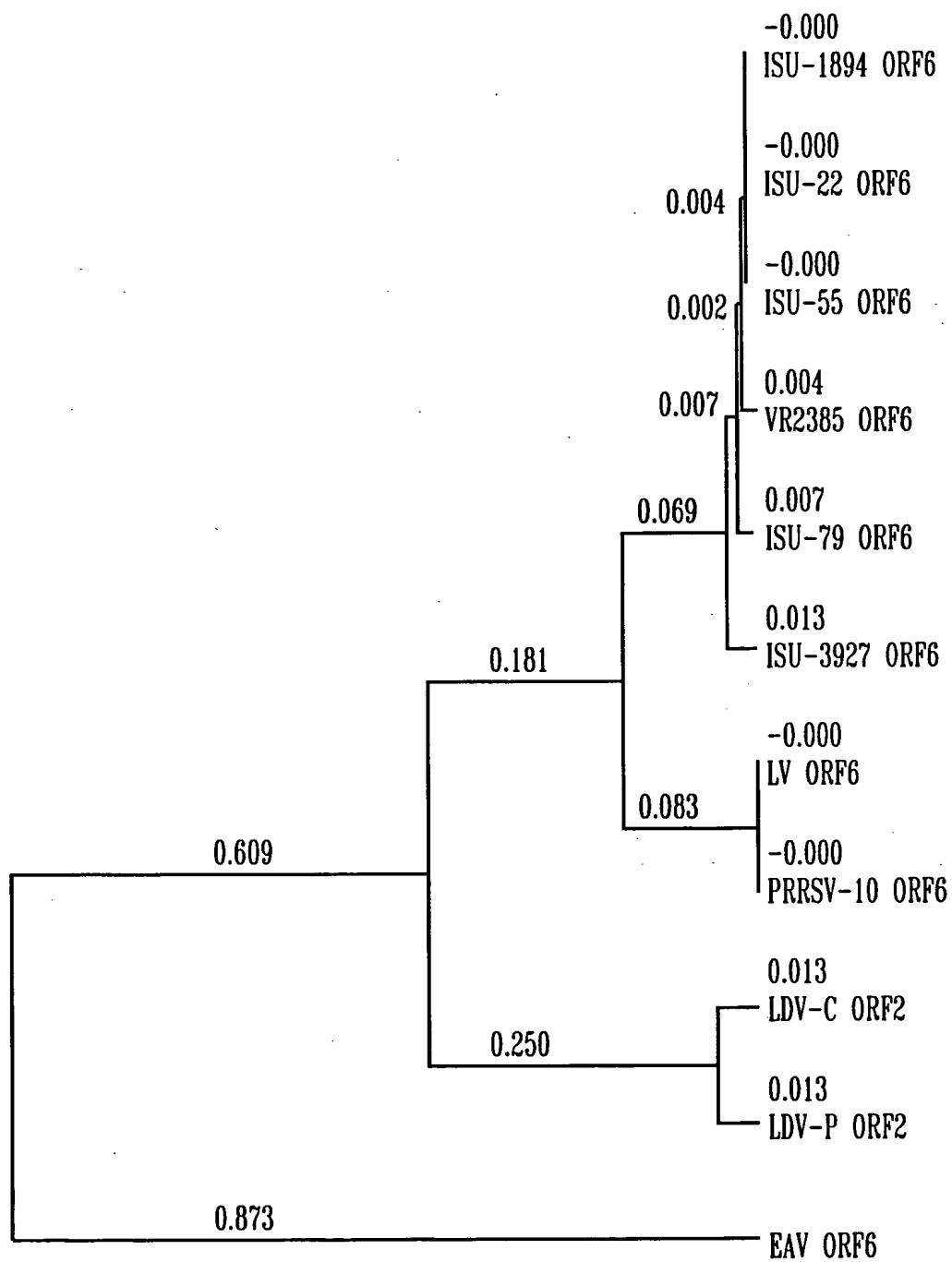


FIG. 19A

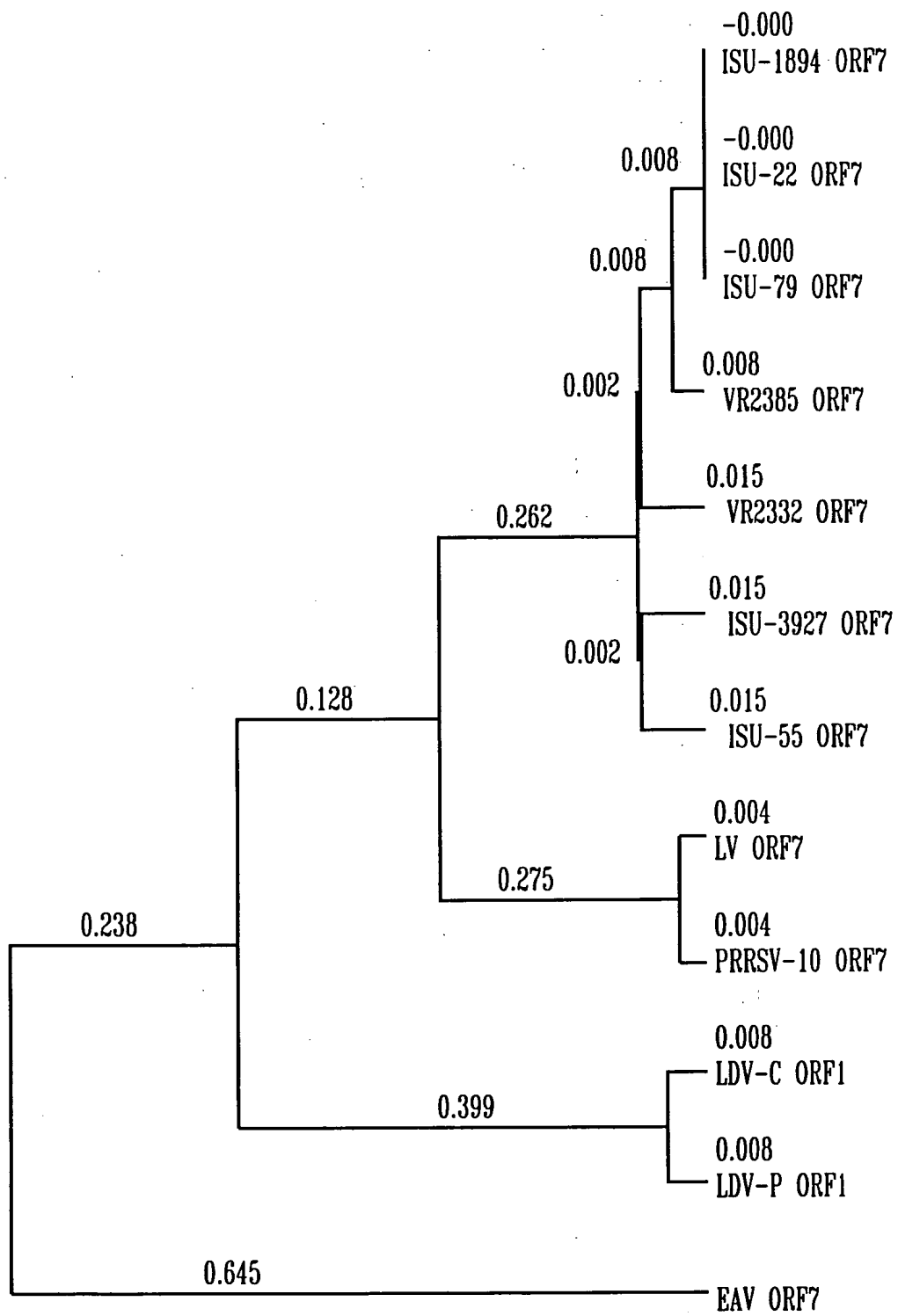


FIG. 19B

+ Start DRF2

100 CCTGAATTGAGATGAAATGGGGTCTATGCAAAAGCCTTTTGGCCAACTTTTGTGGATGCTTTCACGGAGTTCTTGGTGTCATTGTTGAT

200 ATCATTATATTTTGGCCATTTTGTGGCTTACCATCGCAGGTGGCTGGTGGTCTTTTGCATCAGATTGGTTTGGCTCCGGGATACTCCGTGCGCGCC

300 CTGCCATTCACTCTAGCAATTACAGAAATCCTATGAGGCCCTTCTCTCTCAGTGCCAGGTGGACATTCCCACCTGGGGAACATAACATCCTTTGGGGA

400 TGCTTTGGCACCATAAGGTGTCAACCCCTGATTGATGAAATGGTGTGGCTCGAATGTACCGCATCATGGAAAAAGCAGGACAGGCTGCCTGGAAACAGGT

500 AGTGAGCGAGGCTAGCGTGTCTCGCATTAGTAGTTTGGATGTGGTGGCTCATTTTTCAGGCATCTTGGCGCCATTGAAGCCGAGACCTGTAAATATCTGGCC

600 TCTCGGCTGCCCATGCTACACCACCTGGCGATGACAGGGTCAAAATGTAAACCATAGTGTATAATAGTACTTTGAATCAGGTGTTTGGTGTTCCTCCCAACCC

+ Start DRF3

700 CTGGTTCCCGGCCAAAGCTTCATGATTTCCAGCAATGGCTAAATAGCTGTACATTCCTCTATATTTTCTCTGTTCAGCTTCTTGTACTCTTTTGTGTGT

*** Stop DRF2

800 GCTGTGGTTGCGGGTTCCAAATGCTACGTACTGTTTGGTTTCCGCTGGTTAGGGGCAATTTTCTTTCGAACCTACGGTGAAATTACACGGTGTGCCGC

900 CTTGCCTCACCCGGCAAGCAGCCGCAGAGGCCTACGAACCCGGCAGGTCCCTTTGGTGCAGGATAGGGCATGATCGATGTGGGAGGACGATCATGATGA

1000 ACTAGGGTTTGTGGTGGCGTCTGGCCCTCTCCAGCGAAGGCCACTTGACCAGTGTCTACGCCCTGGTTGGCGTCCCTGTCCCTTCAGCTATACGGCCCAAGTTC

1100 CATCCCGAGATATTCGGGGATAGGGAAATGTGAGTCGAGTCTATGTTGACATCAAGCACCATTTCATTTGCGCTGTTTCATGATGGGCAGAACACCACCTTGC

FIG. 20A

+ Start DRF4

CCCACCATGACAACATTTAGCCGTGCTTCAGACCTATTACCAGCATCAGGTCGACGGGGGCAATTGGTTTCACCTAGAATGGTGCGTCCCTTCCTTTTC 1200

CTCTTGGTTGGTTTTAAATGTCCTCTTGGTTTCTCAGGGCTTCGCCTGCAAGCCATGTTTCAGTTCGAGTCTTTTCAGACATCAAGACCAACACCACCGCAG 1300

*** Stop DRF3

CGGCAGGCTTTGCTGTCTCCCAAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCTCTGAGCGGATTTCGCAAAAGTCCCTCAGTGCCGACGGCGATAGG 1400

GACACCCGTGTATATCACTGTCACAGCCAATGTTACCGATGAGAAATTATTTGCATTCCCTCTGATCTTCATGCTTTCTTGCCTTTTCTATGCTTCT 1500

GAGATGAGTGAAAAGGGATTTAAGGTGGTATTTGGCAATGTGTAGGCATCGTGGCAGTGTGGGTCAACTTCACCAGTTACGTCCAACATGTCAAGGAAT 1600

TTACCCAACGTTCCCTTGGTAGTTGACCAIGTGGGCTGCTCCATTTCATGACGCCCGAGACCATGAGGTGGGCAACGTTTTAGCCTGCTCTTTTACCAT 1700

*** Stop DRF4 + Start DRF5

TCGTGGCAATTTGAATGTTTAAGTAAGTGGGGAAATGCTTGACCGGGGCTGTTGCTCGCAATTGCTTTTTTATGGTGTATCGTGCCGCTTGT 1799

FIG. 20B

Consensus	ATGMAATGGGTCWMTGIRRAGCCTTTTGGAYAAAATYRGCCARCTKTTYGTGGAYGCTTACAGAGTTCYTKGTSYRTKGTGATATYRYATWTT	100
VR2385 DRF2	...A...TA...CAA...C...TG...A...T...T...T...G...T...G...GTCCA...T...CATT...A...	100
LV DRF2	...C...AC...TGG...-----T...CA...G...G...C...C...T...T...TAGTG...G...TGCC...T...	91
Consensus	YYTKGCCATWYGTGTTGGSTTACCGTCCGAGGWTGGYTRSTGGTCTTTYKMYTCAGAKTGGTTTGCTCCGGMTWCTCCGTCGCGCYCTGCCATTAC	200
VR2385 DRF2	TT...G...TT...C...A...T...C...GG...TGCA...T...A...A...G...C...	200
LV DRF2	CC...T...AC...G...G...A...T...AC...CTTC...G...C...T...T...T...	191
Consensus	TCTSMSSAAYTAYMGAAGRTCTATGARGCTTKYTSYCYMASTGCMRRSYGGAYAKTCCCACAMTKKSARYAARCAAYCCWTTGGGKATGYTTTGGA	300
VR2385 DRF2	...GAGC...T...CA...A...G...C...TC...CT...TC...G...CAGGT...C...T...-C...GG...G...ACT...A...T...G...C...	299
LV DRF2	...CCCG...C...TC...G...A...G...GT...GC...CA...C...AGACC...T-G...A...TT...C...GTC...G...C...A...T...T...	290
Consensus	CCATRMGAGTKTCMMMCYTGATTGATGARATGGTSTCKCGTCGMATKTACCRSAYCATGGAAAMAWKCAGGWCARGCKGCCCTGGAARCAGGTGTRGKYGA	400
VR2385 DRF2	...AA...G...AAC...C...A...G...G...A...G...GC...T...A...AG...A...G...T...A...A...A...GA...C...	398
LV DRF2	...-...GC...T...CCA...T...G...C...T...C...T...AG...C...C...TT...T...A...G...G...G...TG...T...	389
Consensus	GGCYACGCTSTCWCGMAKYWGTCAGGKYTSGATRTGTRGTRKTRCTATTTCARCACTKCGCGCMRTKGARGCSGAKWICYTGYMRMTWCTSRSCICWCGRC	500
VR2385 DRF2	...T...G...T...C...TTA...-...TT...G...G...G...G...T...T...T...CA...T...A...C...GA...C...TAAA...A...GGC...T...G...	496
LV DRF2	...C...-...C...A...A...GCT...GC...C...A...A...TA...C...G...AG...G...G...TT...T...CCGC...T...CAG...A...A...	487

FIG. 21A

Consensus	TSSYSATGCTAMAMMAYCTGYGCAYGWAGGGTCAAAATGTRASCMTASWGTAYAAAYASYACKTTGRAYCRSGTGKWKGTCTRTYTTCCCMACSCCNGGTW	600
VR2385 DRF2	.GCCC.....C.CC.C...C...T.AC.....A.C.A..GT...T..T.GT...T...A.T.AG...TT...-G.T.....A..C..T...T	595
LV DRF2	.CGTG.....A.AA.T...-T...-C.TT--...-.....G.G.C..CA...C..C.CC..G...G.C.GC..-GA.....A.C.....C..G..A...A	580
Consensus	CSMGGCCMAAGYTKMMYGATTTCMRRCATGGCTMATMRSTGRCAYKCYTCYATWTTTCCCTCTGKGCWKCTCKKTACYYTKTYYRTWGTGCTKIG	700
VR2385 DRF2	.CC....A...C.TCAT.....CAG.....A..AGC...A..TT.C..T..A.....T...AG.T...TG...TC..TG.T.....G..	695
LV DRF2	.GA...C...T.GACC.....AGA.....C..CAG...G..CG.T..C..T.....G..TT.A...GT...CT.G..CA.A.....T..	680
Consensus	GYTKCGRRTTCCARYKCTACGYWMTGTTTTTGGTTCCRYTGGYMRSGGCAAYWYWTCTTCGARCTSACGGTGA	776
VR2385 DRF2	.T.G..GG....ATG....TAC.....GC...TTAGG....TTTT..T.....A..C.....	771
LV DRF2	.C.T..AA....GCT.....CTA.....AT...CCCAC.....CACA..A.....G..G..-----	750

FIG. 21A. 1

Consensus	ATGGCTMATMRSTGTRCAYKCYTCYATWTTTTCCTCTGTGKGCWKWCCTKKTACYYTKTTRTWGTGCTKGGYTKCGRRTTCCARYKCTACGYWMTGTT	100
LV DRF3C..CAG...G..CG.T..C..T.....G..TT.A...GT...CT..G..CA.A....T...C.T..AA.....GCT.....CTA....	100
VR2385 DRF3A..AGC...A..TT.C..T..A.....T..AG.T...TG...TC.T..TG.T.....G...T.G..GG.....ATG.....TAC....	100
Consensus	TTTGGTTTCCRYTGGYMRSGGCAAYWWTCTTCGARCTSACRSRTSAAYTACACSRTRTGCMYGCCYTGYYACCMGKCAAGCRGCTCGCMRARGSCT	200
LV DRF3AT...CCCAC.....CACA..A.....G..G..CA.C..C.....CA.A...AT...C..TTCI...A.T.....G.....CA.A.G..	200
VR2385 DRF3GC...TTAGG.....TTTT..T.....A..C..GG.G..T.....GG.G...CC...T..CCTC...C.G.....A..-...AG.G.C..	199
Consensus	ACGARCCCGGYMGKWMCMTKTGGTGCARRATAGGGCATGAYMGRGTGTGRGGAGSRYGAYCATGATGARYTAGKKWWTGTCSTSCCGTCYGGSYWCKMCA	300
LV DRF3	-...G.....TC.TAA.A.G.....AA.....CA.G....A....CGT...C.....GT..-..TTAA...CA.C.....C..GTA.GA..	298
VR2385 DRF3	...A.....CA.GTC.C.T.....GG.....TC.A....G....GAC..T.....AC...GGTT...-GG.G....T..CCT.TC..	298
Consensus	sRCGAMKSMMACTTGACSRGTMKTAYGCTGGYTGCGKTYYYTGTCCTYWSCTAYRCGGCCARTTCCATCCSGAGWTRTTCGGGATAGGAATGTGWS	400
LV DRF3	A.--CTCAA.....-GG..TA...T..T...C...T.TTT.....TTC...CG.....A.....G...T.G.....TC	395
VR2385 DRF3	G...AGGCC.....CA..GC...C..C...T....G.CCC.....CAG...TA.....G.....C...A.A.....AG	398
Consensus	KCGMGCTWYGTGACAWSMRRCACCARTTCATTGTGCGYGVKWCATGATGGRCASAAAYWCMACKTRYCYMMSRWSACAACATYTCMGCMKTRYWTSMG	500
LV DRF3	G..C....TC..G....AGCGA....G.....T..C.AG.....T..C..AG.....A..C..TT.A...G.AT.TAC.GGAC.....C..C..AT.ATA.GC.	495
VR2385 DRF3	T..A....AT..T....TCAAG....A.....C..T.TT.....G..G..CA.C...T.GC.CCA.CATG.....T..A..CG.GCT.CA.	498

FIG. 21B

Consensus	RCMTATTACCASCAYCARRTMGACGGGGGCAATTGGTTYCAYYTRGATGGSTGGCKCCMYTCTTTTCYTCYTGGTGTYTMAAYRTMTCWTGGTTTC	600
LV DRF3	G, A, C, . C, . AA, A, C, . TT, G, C, G, . AC, T, . C, GC, C, . CA, A, . A,	595
VR2385 DRF3	A, C, G, . T, . GG, C, T, . CC, A, G, T, . CT, C, . T, TT, A, . TG, C, . T,	598
Consensus	TSAGGGGTTCCGCTGYAAGCCMTGTTTCWSKWCGRCTCTWTGAGAYATYRAGACCACACACACCGCRGCKGCMGGYTTYRYKGTCTCTYCARGACATCART	700
LV DRF3	, G, T, TCGA, . CA, . . A, T, . TG, G, G, . T, . C, . T, . . CATG, T, . G, A, .	695
VR2385 DRF3	, C, C, A, AGTT, . AG, . . T, C, . CA, C, A, . G, . A, . C, . TGCT, C, . A, G, .	698
Consensus	TGYYTYMGRCMTCACGGSRWCTCRGCAGCKCAWGAGRMRAATTCCTTCGSAAGTCGYCYCARTGYCGYGAMGCGWYRGTACTCCCCAGTACATCACGA	800
LV DRF3	, . TT, CC, A, C, GGT, . . A, G, . A, . . AAA, G, T, C, . A, . T, . . A, C, . TCG,	795
VR2385 DRF3	, . CC, TA, G, A, . ---, CAA, . . G, . --, T, . -T, GCG, . ----, C, -C, T, . G, . C, . C-, C, G, . ATA, . ----	765
Consensus	TAA	803
LV DRF3	. . .	798
VR2385 DRF3	---	765

FIG. 21B.1

Consensus	M. WG. C., K., L., W., L., SL., P., CL., SPSQ., G., WSF., S., WFAPR., SVRALPFTL, NYRRSYE., L., C., D., P., KH	100
LV DRF2,	. Q., H., GV., SASCSWTPS., SSLLV., LI-----, PF., ---, Y., G., D., Y., F., E., F., P., GL., PN., RP., V., QFAV.,	90
VR2385 DRF2,	. K., L., --, -----AFLTK., AN-FL., MLSSSWCP., LI., YFW., F., A., V., W., A., D., Y., S., AF., SQ., QV., I., TWGT.,	93
Consensus	PLGM., WH., VS., LIDEMVSR., Y., ME., GGAANKQV., EATL., S., LD., V., HFQHLAA., EA., C., L., SRL., ML., NV., YN., TL., V.,	200
LV DRF2, F., MR., H., I., QT., HS., G., TKL., G., I., T., V., DS., RF., S., V., KN., AV--G., SLQ., T., DR., ELI	188
VR2385 DRF2, L., HK., T., M., RI., KA., S., SRI., S., V., A., I., ET., KY., A., P., HH., RMTGS., TIV., S., NQ., FAV	193
Consensus	FPTPG., RPKL., DF., QWLI., VH., SIFSSVA., S., TLF., VLWLR., P., LR., VEGF., W., A.,	264
LV DRF2, T., T., R., S., A., S., V., I., I., A., Y., H., PT., ---THSS	249
VR2385 DRF2, S., H., Q., A., S., A., C., V., V., M., T., R., LG., IFLSNSR-	257

FIG. 22A

Consensus	MA, C,	FLC,	Y,	A,	S,	T, CFWFPL,	GN, SFELT, NYT, C, PC, T, QAA,	EPGR,	WC, IGHDRC, E, DHDEL,	PSG,	100	
LV DRF3,	HQ, ARFHF,	GFIC, LVHS, LASN, SS, L,	AH,	T,	I,	I, M, S, S,	RQRL,	NM, K,	E, R,	LMSI,	YDN 100
VR2385 DRF3,	NS, TFLYI,	CSFL, SFCC, VVAG, NA, Y,	VR, F,	V,	V, P, L, R,	AEAY,	SL, R,	G, D,	GFVV,	LSS 100	
Consensus	L,	YAWLA, LSFSY, AQFHPE, FGIGNVSRV, VD,	HQFICA, HDG, N, T,	NISA,	YY, HQ, DGGNWFHLEW, RP, FSSWLVLN, SWFL	200					
LV DRF3,	L-K, EGY,	F,	A,	L,	F, KR,	E, H, S, VSTGH,	LYAA, H, I,	L, L,	I,	199	
VR2385 DRF3,	EGH, TSA,	S,	T,	I,	Y, IK,	V, Q, T, LPHHD,	VLQT, Q, V,	V, F,	V,	200	
Consensus	RRSP, S, VS, R, Q, RPT, P,	S,	TS,	L,	R, F,	K, S,				266	
LV DRF3,	V, P, R, IY, IL,	R, RLPVSW, FR,	IVSD, TGSQQRK, K, PSESPPNVV, P, VLPSTSR						265	
VR2385 DRF3,	A, H, V, VF, TS,	P, QRQALL, SK, V--A, GIATRPL, R, A-----, - , LSAARR-							255	

FIG. 22B

Consensus	M, A,	LF, L, G,	VS, AFACKPCFS,	LSDI, TINTAAAGF, VLQDI, C, R,	A, E, I,	K, QCR, A, GTP, YIT, TANVTDE, YL,	DL 100				
LV DRF4,	A, AT,	F, A, AQHIM, E,	TH,	E,	M,	N, F, PHGVSA, Q, K, SFG, SS,	E, V,	Q, I,	S, YNA,	100
VR2385 DRF4,	G, SL,	L, V, FKCLL, Q,	SS,	K,	A,	S, L, HR--NS, S, A, R--, VP,	T, I,	V,	N, HSS,	96
Consensus	LMLS, CLFYASEMSEKGFV, FGNVSG, V,	CVNFT, YV, HV,	TQ,	V,	RLHF, TP, MRWAT,	ACLF, ILLAI,				184
LV DRF4,	A,	I,	V, SA,	D, A, TQH, QHHL, IDHI,	L, SA,	TI,	A,	183
VR2385 DRF4,	S,	V,	I, AV,	S, Q, KEF, RSLV, DH-V,	M, ET,	VL,	T,	179

FIG. 22C

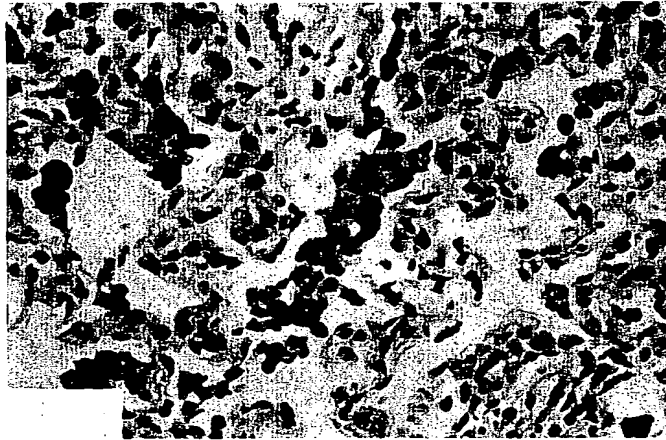


FIG.23

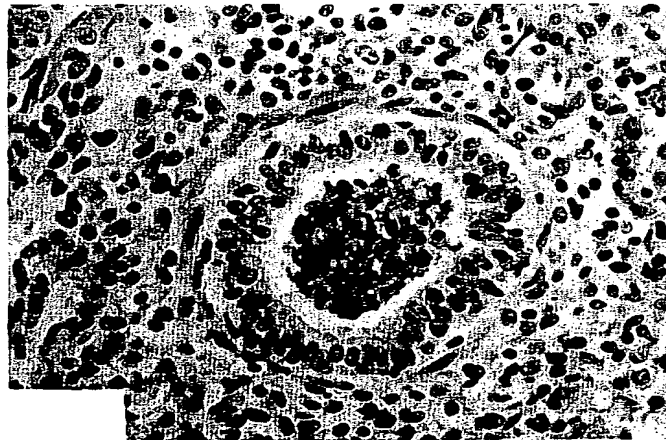


FIG.24

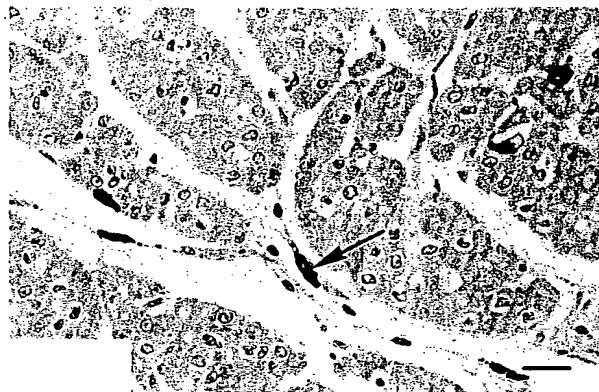


FIG.25

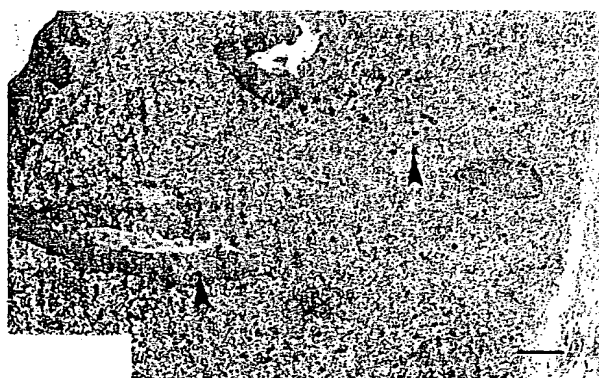


FIG.26

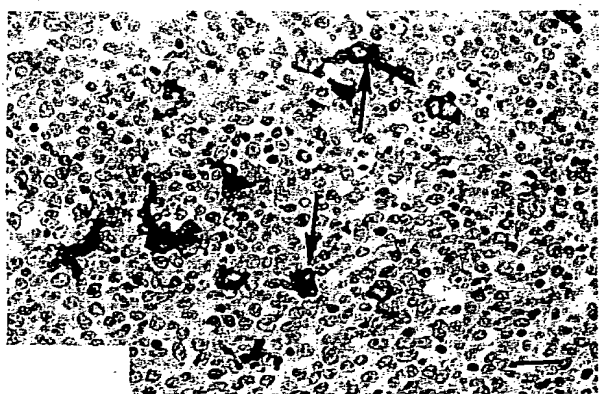


FIG.27



FIG. 28A

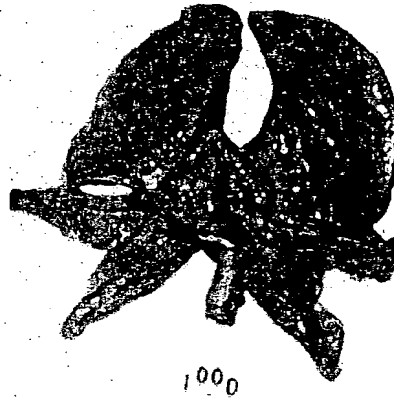


FIG. 28B

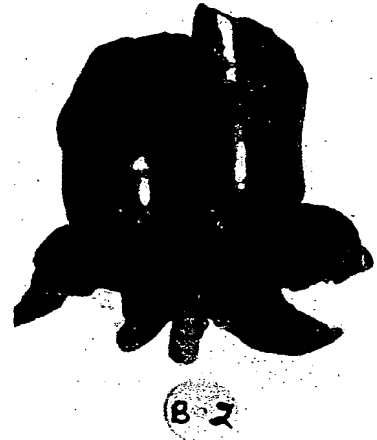


FIG. 28C

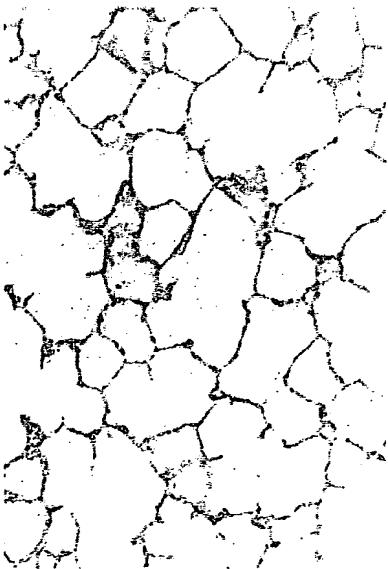


FIG. 29A

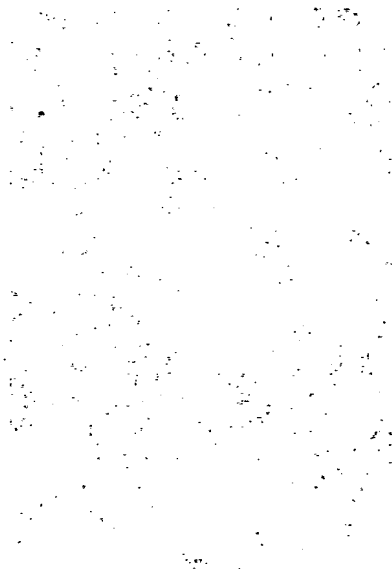
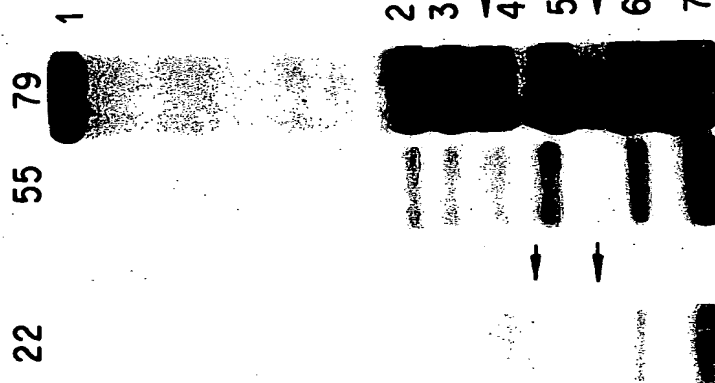


FIG. 29B



FIG. 29C

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2 3 4 5 6 7

FIG.30A

FIG.30B

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